



APR 25 2002

TECH CENTER 1600/2900

SEQUENCE LISTING

<110> Yang, Chu-Wen
Tsou, Ann-Ping
Chi, Chin-Wen
Fann, Ming-Ji
Chou, Chen-Kung

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• 210> 2

• 211> 808

• 212> PRT

• 213> Mus musculus

• 400> 2

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  35              40              45
Asp Val Asn Ile Pro Leu Glu Gly Arg Glu Leu Gly Asn Ile His Glu
  50              55              60
Thr Ser Gln Asp Leu Ser Pro Glu Lys Ala Ser Ser Lys Thr Arg Ser
  65              70              75              80
Val Lys Met Val Leu Ser Asp Gln Arg Lys Gln Leu Leu Gln Lys Tyr
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Lys Glu Glu Lys Gln Leu Gln Lys Leu Lys Glu Gln Arg Glu Lys Ala
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Asp Gln Arg Gln Thr Ser Glu Lys Gln Pro Leu Asp Arg Glu Arg Lys
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Lys Val Ile Pro Ser Lys Val Glu Arg Asp Glu Lys His Leu Asp Ser
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 Asp Leu Ile Leu Phe Ser Pro Leu
 805

4210 • 3
 4211 • 2538
 4212 • DNA
 4213 • Homo sapiens

4400 • 3
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2538

0210: 4

0211: 846

0212: PRT

0213: Homo sapiens

0400: 4

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Ala	Met	Lys	Thr	Ile	Leu	Gly	Asp	Gln	Arg	Lys	Gln	Met	Leu	Gln	Lys
				85					90					95	
Tyr	Lys	Glu	Glu	Lys	Gln	Leu	Gln	Lys	Leu	Lys	Glu	Gln	Arg	Glu	Lys
		100						105					110		
Ala	Lys	Arg	Gly	Ile	Phe	Lys	Val	Gly	Arg	Tyr	Arg	Pro	Asp	Met	Pro
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Ala	Ile	Pro	Ser	Ser	Val	Arg	Ile	Thr	Arg	Ser	Lys	Ala	Lys	Asp	Gln
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 420 425 430
 Phe Arg Asn Ile Leu Gln Ser Glu Thr Glu Lys Leu Thr Ser His Cys
 435 440 445
 Phe Glu Trp Asp Arg Lys Leu Glu Leu Asp Ile Pro Asp Asp Ala Lys
 450 455 460
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 465 470 475 480
 Arg Phe Lys Gln Phe Glu Gly Leu Val Asp Asp Cys Glu Tyr Lys Arg
 485 490 495
 Gly Ile Lys Glu Thr Thr Cys Thr Asp Leu Asp Gly Phe Trp Asp Met
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 595 600 605
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 Gly Leu Ser Val Ser Ser Glu Gly Pro Ser Gln Arg Leu Gly Thr Pro
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 Ser Glu His Val Lys Lys Thr Leu Phe Leu Ser Ile Pro Glu Ser Arg
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 Ser Glu Arg Met Ser Leu Pro Leu Leu Ala Gly Gly Val Ala Asp Asp
 725 730 735
 Ile Asn Thr Asn Lys Lys Glu Gly Ile Ser Asp Val Val Glu Gly Met
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 Glu Lys Asn Thr Ala Ser Gln Asn Ser Ile Leu Glu Glu Gly Glu Thr
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 Lys Ile Ser Gln Ser Glu Leu Phe Asp Asn Lys Ser Leu Thr Thr Glu
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 Cys His Leu Leu Asp Ser Pro Gly Leu Asn Cys Ser Asn Pro Phe Thr
 805 810 815
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 Gly Asn Leu Ile Thr Phe Ser Pro Leu Gln Pro Gly Glu Phe
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*210> 5
 *211> 2966
 *212> DNA
 *213> Mus musculus

*220>
 *221> CDS
 *222> (301)...(2724)

*400> 5

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Glu Asn Arg His Arg Val Tyr Glu Arg Asn Arg His Phe Gly Leu Lys						
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Asp Val Asn Ile Pro Leu Glu Gly Arg Glu Leu Gly Asn Ile His Glu						
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Thr Ser Gln Asp Leu Ser Pro Glu Lys Ala Ser Ser Lys Thr Arg Ser						
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Val Lys Met Val Leu Ser Asp Gln Arg Lys Gln Leu Leu Gln Lys Tyr						
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Asp Gln Arg Gln Thr Ser Glu Lys Gln Pro Leu Asp Arg Glu Arg Lys	180	185	190	
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Val Met Gln Pro Val Leu Phe Thr Ser Gly Lys Gly Thr Glu Ser Ala	195	200	205	
gct act cag aga ggc aag ctg atg gcc cga aca gtg tca tcc act aca				972
Ala Thr Gln Arg Ala Lys Leu Met Ala Arg Thr Val Ser Ser Thr Thr	210	215	220	
aga aag cca gtc aca aga gcc acg aat gag aaa gga tca gaa aga atg				1020
Arg Lys Pro Val Thr Arg Ala Thr Asn Glu Lys Gly Ser Glu Arg Met	225	230	235	240
aga cca agt gga ggg aga cct gcc aaa aaa cca gaa ggc aag ccg gac				1068
Arg Pro Ser Gly Gly Arg Pro Ala Lys Lys Pro Glu Gly Lys Pro Asp	245	250	255	
aag gtc att cct tcc aaa gtt gag cgg gac gaa aag cat ttg gat tgg				1116
Lys Val Ile Pro Ser Lys Val Glu Arg Asp Glu Lys His Leu Asp Ser	260	265	270	
cag acc agg gaa aca agt gaa atg ggt ctg ctg gga gtc ttc cga gaa				1164
Gln Thr Arg Glu Thr Ser Glu Met Gly Leu Leu Gly Val Phe Arg Glu	275	280	285	
gtg gaa agc ttg cct gca aca gcc cct gcc caa gga aag gaa agg aag				1212
Val Glu Ser Leu Pro Ala Thr Ala Pro Ala Gln Gly Lys Glu Arg Lys	290	295	300	
tcc ttt gcc ccc aag cac tgt gtc ttc cag ccc ccg tgt ggt ctg aag				1260
Ser Phe Ala Pro Lys His Cys Val Phe Gln Pro Pro Cys Gly Leu Lys	305	310	315	320
agc tac cag gtg gct ccc ctg agc cct aga agt gcc aac gct ttc ctg				1308
Ser Tyr Gln Val Ala Pro Leu Ser Pro Arg Ser Ala Asn Ala Phe Leu	325	330	335	
aca ccc aat tgt gat tgg aac cag tta aga cca gaa gtt ttt agc act				1356
Thr Pro Asn Cys Asp Trp Asn Gln Leu Arg Pro Glu Val Phe Ser Thr	340	345	350	
aca act caa gac aaa gca aat gaa atc ttg gta cag caa gga ttg gag				1404
Thr Thr Gln Asp Lys Ala Asn Glu Ile Leu Val Gln Gln Gly Leu Glu	355	360	365	
tgg cta aca gac cgt agt aaa gaa cat gtc tta aat cag aag ggc gct				1452
Ser Leu Thr Asp Arg Ser Lys Glu His Val Leu Asn Gln Lys Gly Ala	370	375	380	
tct act tca gat tca aat cac gct tct gtg aaa gga gtc cca tgc tct				1500
Ser Thr Ser Asp Ser Asn His Ala Ser Val Lys Gly Val Pro Cys Ser				

385	390	395	400	
gaa ggg agc gaa ggc cag acc tct cag ccc ccc ccc gat gtg cca tac				1548
Glu Gly Ser Glu Gly Gln Thr Ser Gln Pro Pro His Asp Val Pro Tyr				
405		410	415	
ttc aga aaa atc ctc caa tca gaa act gac agg ctg acc tgg ccc tgc				1546
Phe Arg Lys Ile Leu Gln Ser Glu Thr Asp Arg Leu Thr Ser His Cys				
420		425	430	
ctg gag tgg gag ggg aag ctg gac ctg gac atc tct gat gaa gct aaa				1644
Leu Glu Trp Glu Gly Lys Leu Asp Leu Asp Ile Ser Asp Glu Ala Lys				
435		440	445	
ggt ctt atc cgt acc aag gtt ggt caa caa aga ctc ctt atc aag gag				164
Gly Leu Ile Arg Thr Thr Val Gly Gln Thr Arg Leu Leu Ile Lys Glu				
450		455	460	
aga ttc aga cag ttt gaa gga ctg gtg gac aac tgc gag tat aaa cgg				1740
Arg Phe Arg Gln Phe Glu Gly Leu Val Asp Asn Cys Glu Tyr Lys Arg				
465		470	475	480
ggt gaa aag gag aag acc tgc acc gat ctg gat gga ttc tgg gat atg				178
Gly Glu Lys Glu Thr Thr Cys Thr Asp Leu Asp Gly Phe Trp Arg Met				
485		490	495	
gtt agt ttt cag gtc gat gat gtg aac cag aaa ttc aac aac ctg atc				1836
Val Ser Phe Gln Val Asp Asp Val Asn Gln Lys Phe Asn Asn Leu Ile				
500		505	510	
aaa ctt gag ggc tca gga tgg aaa gac agc aat aat cca agc aaa aaa				1884
Lys Leu Glu Ala Ser Gly Trp Lys Asp Ser Asn Asn Pro Ser Lys Lys				
515		520	525	
gtc ctc cgg aaa aaa att gtg cct ggt aga aba agc aaa gca aag cag				1932
Val Leu Arg Lys Lys Ile Val Pro Gly Arg Thr Ser Lys Ala Lys Gln				
530		535	540	
gat gac gac gga cga ggc gca gct agg agt cgc ctt gct gcc ata aag				1980
Asp Asp Asp Gly Arg Ala Ala Ala Arg Ser Arg Leu Ala Ala Ile Lys				
545		550	555	560
aat gca atg aaa ggc agg cca cag cag gaa gtg cag gcc ccc gca gca				2028
Asn Ala Met Lys Gly Arg Pro Gln Gln Glu Val Gln Ala His Ala Ala				
565		570	575	
gct cgg gag acc aba aag gaa gtt gac aaa ata gtg ttt gac gct ggg				2076
Ala Pro Glu Thr Thr Lys Glu Val Asp Lys Ile Val Phe Asp Ala Gly				
580		585	590	
ttt ttc aga atc gag agc cca gtg aag tca ttc tca gtc ctg tct tct				2124
Phe Phe Arg Ile Glu Ser Pro Val Lys Ser Phe Ser Val Leu Ser Ser				
595		600	605	
gaa cgt cgt tct caa aga ttt gga acc cct ctg cct gcc agc aaa gtt				2172
Glu Arg Arg Ser Gln Arg Phe Gly Thr Pro Leu Ser Ala Ser Lys Val				
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Val Pro Glu Gly Arg Ala Ala Gly Asp Leu Leu Arg Gln Lys Met Pro
625 630 635 640

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Leu Lys Lys Pro Asp Pro Gln Ser Ser Lys Ser Glu His Val Asp Arg
645 650 655

acg ttt tca gat ggt ctt gaa agc agg ttc cac gta gaa gac acc ccc 2316
Thr Phe Ser Asp Gly Leu Glu Ser Arg Cys His Val Glu Asp Thr Pro
660 665 670

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Cys Pro Gly Glu Gln Asp Ser Ser Asp Ile Glu His Asp Val Asn Lys
675 680 685

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Ile Asn Val Lys Met Asp Cys Phe Ser Val Glu Thr Asn Leu Pro Leu
690 695 700

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725 730 735

cct gag aca aat acc tcc tca cag agc aac acc tca caa gaa gaa gct 2556
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740 745 750

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Glu Ala Ser Gln Ser Val Leu Leu His Lys Ser Leu Thr Ser Glu Cys
755 760 765

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His Leu Leu Glu Pro Pro Gly Leu Ser Cys Thr Ser Pro Cys Thr Arg
770 775 780

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Glu Glu Thr Arg Gln Pro Asp Arg Ser Arg Gln Phe Ser Phe Gly Gly
785 790 795 800

gac ctc att ctc ttc tca caa cta tgaccctgaa gggaacacca ggagggcttt 2754
Asp Leu Ile Leu Phe Ser Pro Leu
805

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<211> 2979

<212> DNA

0213 > Homo sapiens

0220 >

0221 > CDS

0222 > (218)...(2755)

0400 > 6

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tgtgagggtt	cctgcttggg	agtcggcggt	ggctgctcag	accgagtgtt	ctttactttt	180
tggttggttg	aggtttcagc	ctagaagggtg	gctcagg	atg	tct	235
				Met	Ser Ser Ser His Phe	
				1	5	

gpc	agt	cga	cac	agg	aag	gat	ata	agt	act	gaa	atg	att	aga	act	aaa	283
Ala	Ser	Arg	His	Arg	Lys	Asp	Ile	Ser	Thr	Glu	Met	Ile	Arg	Thr	Lys	
			10					15					20			

att	gct	cat	agg	aaa	tca	ctg	tct	cag	aaa	gaa	aat	aga	cat	aag	gaa	331
Ile	Ala	His	Arg	Lys	Ser	Leu	Ser	Gln	Lys	Glu	Asn	Arg	His	Lys	Glu	
		25					30					35				

tac	gaa	cga	aat	aga	cac	ttt	ggg	ttg	aaa	gat	gta	aac	att	cca	acc	379
Tyr	Glu	Arg	Asn	Arg	His	Phe	Gly	Leu	Lys	Asp	Val	Asn	Ile	Pro	Thr	
	40					45					50					

ttg	gaa	ggg	aga	att	ctt	gtt	gaa	tta	gat	gag	aca	tct	caa	gag	ctt	427
Leu	Glu	Gly	Arg	Ile	Leu	Val	Glu	Leu	Asp	Glu	Thr	Ser	Gln	Glu	Leu	
	55				60				65					70		

gtt	cca	gaa	aag	aac	aat	gtt	aag	cca	arg	gca	atg	aaa	act	att	cta	475
Val	Pro	Glu	Lys	Thr	Asn	Val	Lys	Pro	Arg	Ala	Met	Lys	Thr	Ile	Leu	
			75					80						85		

ggg	gat	caa	cga	aaa	cag	atg	ctc	caa	aaa	tac	aaa	gaa	gaa	aag	caa	523
Gly	Asp	Gln	Arg	Lys	Gln	Met	Leu	Gln	Lys	Tyr	Lys	Glu	Glu	Lys	Gln	
		90					95					100				

ctt	caa	aaa	ttg	aaa	gag	cag	aga	gag	aaa	gct	aaa	cga	gga	ata	ttt	571
Leu	Gln	Lys	Leu	Lys	Glu	Gln	Arg	Glu	Lys	Ala	Lys	Arg	Gly	Ile	Phe	
		105					110					115				

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Lys	Val	Gly	Arg	Tyr	Arg	Pro	Asp	Met	Pro	Cys	Phe	Leu	Leu	Ser	Asn	
	120					125					130					

cag	aat	gct	gtg	aaa	gct	gag	cca	aaa	aag	gct	att	cca	tct	tct	gta	667
Gln	Asn	Ala	Val	Lys	Ala	Glu	Pro	Lys	Lys	Ala	Ile	Pro	Ser	Ser	Val	
	135				140				145						150	

cgg	att	aca	agg	tca	aag	goc	aaa	gac	caa	atg	gag	cag	act	aag	att	715
Arg	Ile	Thr	Arg	Ser	Lys	Ala	Lys	Asp	Gln	Met	Glu	Gln	Thr	Lys	Ile	
			155					160						165		

gat	aac	gag	agt	gat	gtt	cga	gca	atc	cga	cct	ggg	cca	aga	caa	act	763
Asp	Asn	Glu	Ser	Asp	Val	Arg	Ala	Ile	Arg	Pro	Gly	Pro	Arg	Gln	Thr	
			170					175						180		

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Ser Glu Lys Lys Val Ser Asp Lys Glu Lys Lys Val Val Gln Pro Val	
185 190 195	
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Met Pro Thr Ser Leu Arg Met Thr Arg Ser Ala Thr Gln Ala Ala Lys	
200 205 210	
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Gln Val Pro Arg Thr Val Ser Ser Thr Thr Ala Arg Lys Pro Val Thr	
215 220 225 230	
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Arg Ala Ala Asn Glu Asn Glu Pro Glu Gly Lys Val Pro Ser Lys Gly	
235 240 245	
aga cct gcc aaa aat gta gaa aca aaa ccc gac aag ggt att tct tgt	1003
Arg Pro Ala Lys Asn Val Glu Thr Lys Pro Asp Lys Gly Ile Ser Cys	
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Lys Val Asp Ser Glu Glu Asn Thr Leu Asn Ser Gln Thr Asn Ala Thr	
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Ser Gly Met Asn Pro Asp Gly Val Leu Ser Lys Met Glu Asn Leu Pro	
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Glu Ile Asn Thr Ala Lys Ile Lys Gly Lys Asn Ser Phe Ala Pro Lys	
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315 320 325	
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Pro Met Thr Pro Arg Ser Ala Asn Ala Phe Leu Thr Pro Ser Tyr Thr	
330 335 340	
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Trp Thr Pro Leu Lys Thr Glu Val Asp Glu Ser Gln Ala Thr Lys Glu	
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Ile Leu Ala Gln Lys Cys Lys Thr Tyr Ser Thr Lys Thr Ile Gln Gln	
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Asp Ser Asn Lys Leu Pro Cys Pro Leu Gly Pro Leu Thr Val Trp His	
375 380 385 390	
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Glu Glu His Val Leu Asn Lys Asn Glu Ala Thr Thr Lys Asn Leu Asn	
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 680 685 690
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 Gln Cys Pro Gly Leu Pro Asp Leu Ile Glu Glu Asn His Val Val Asn
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Or fude